RAW SEQUENCE LISTING   DATE: 06/08/2001
PATENT APPLICATION: **US/09/864,169**   TIME: 16:45:24

Input Set : **A:\208377.txt**
Output Set: **N:\CRF3\06082001\I864169.raw**   ENTERED

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   3 <110> APPLICANT: IMAEDA, TAKAO
   4        YAMADA, YUKIO
   5        HIRAI, MASANA
   6        SHIMAMURA, TAKASHI
   7        KOHDA, KATSUNORI
   8        MURAMOTO, NOBUHIKO
  10 <120> TITLE OF INVENTION: METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION
PROTEIN
  12 <130> FILE REFERENCE: 208377USO
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/864,169
C--> 14 <141> CURRENT FILING DATE: 2001-05-25
  14 <150> PRIOR APPLICATION NUMBER: JP2000-161090
  15 <151> PRIOR FILING DATE: 2000-05-26
  17 <160> NUMBER OF SEQ ID NOS: 12
  19 <170> SOFTWARE: PatentIn version 3.0
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 392
  23 <212> TYPE: DNA
  24 <213> ORGANISM: Hordeum vulgare
  26 <220> FEATURE:
  27 <221> NAME/KEY: CDS
  28 <222> LOCATION: (1)..(390)
  30 <400> SEQUENCE: 1
  31 gaa aag cat atg att gaa ggt cgt atg aaa agc tgc tgc cgt agc acc     48
  32 Glu Lys His Met Ile Glu Gly Arg Met Lys Ser Cys Cys Arg Ser Thr
  33 1               5                  10                  15
  35 ctg ggt cgt aac tgc tat aac ctg tgc cgt gtt cgt ggt gcg cag aaa     96
  36 Leu Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys
  37             20                  25                  30
  39 ctg tgc gcg ggt gtt tgc cgt tgc aaa ctg acc agc agc ggt aaa tgc    144
  40 Leu Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys
  41         35                  40                  45
  43 ccg acc ggt ttt ccg aaa atg att gaa ggt cgt acg ctg gcg ctg gtt    192
  44 Pro Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Thr Leu Ala Leu Val
  45     50                  55                  60
  47 agc aac agc gat gaa ccg gat acc gtt aaa tat tgc aac ctg ggt tgc    240
  48 Ser Asn Ser Asp Glu Pro Asp Thr Val Lys Tyr Cys Asn Leu Gly Cys
  49 65                  70                  75                  80
  51 cgt gcg agc atg tgc gat tat atg gtt aac gcg gcg gcg gat gat gaa    288
  52 Arg Ala Ser Met Cys Asp Tyr Met Val Asn Ala Ala Ala Asp Asp Glu
  53                 85                  90                  95
  55 gaa atg aaa ctg tat ctg gaa aac tgc ggt gat gcg tgc gtt aac ttt    336
  56 Glu Met Lys Leu Tyr Leu Glu Asn Cys Gly Asp Ala Cys Val Asn Phe
  57             100                 105                 110
  59 tgc aac ggt gat gcg ggt ctg acc agc ctg acc gcg tga tag gat ccg    384
  60 Cys Asn Gly Asp Ala Gly Leu Thr Ser Leu Thr Ala     Asp Pro
  61         115                 120                     125
  63 gct gct aa                                                          392
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/864,169

DATE: 06/08/2001
TIME: 16:45:24

Input Set : A:\208377.txt
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 64 Ala Ala
 68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 124
 70 <212> TYPE: PRT
 71 <213> ORGANISM: Hordeum vulgare
 73 <400> SEQUENCE: 2
 75 Glu Lys His Met Ile Glu Gly Arg Met Lys Ser Cys Cys Arg Ser Thr
 76 1               5                   10                  15
 79 Leu Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys
 80              20                  25                  30
 83 Leu Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys
 84          35                  40                  45
 87 Pro Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Thr Leu Ala Leu Val
 88      50                  55                  60
 91 Ser Asn Ser Asp Glu Pro Asp Thr Val Lys Tyr Cys Asn Leu Gly Cys
 92 65                  70                  75                  80
 95 Arg Ala Ser Met Cys Asp Tyr Met Val Asn Ala Ala Ala Asp Asp Glu
 96              85                  90                  95
 99 Glu Met Lys Leu Tyr Leu Glu Asn Cys Gly Asp Ala Cys Val Asn Phe
100              100                 105                 110
103 Cys Asn Gly Asp Ala Gly Leu Thr Ser Leu Thr Ala
104          115                 120
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 4
109 <212> TYPE: PRT
110 <213> ORGANISM: Hordeum vulgare
112 <400> SEQUENCE: 3
114 Asp Pro Ala Ala
115 1
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 1649
120 <212> TYPE: DNA
121 <213> ORGANISM: Hordeum vulgare
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (1)..(1647)
127 <400> SEQUENCE: 4
128 gac aag cat atg att gaa ggt cgt aaa agc tgc tgc cgt agc acc ctg       48
129 Asp Lys His Met Ile Glu Gly Arg Lys Ser Cys Cys Arg Ser Thr Leu
130 1               5                   10                  15
132 ggt cgt aac tgc tat aac ctg tgc cgt gtt cgt ggt gcg cag aaa ctg       96
133 Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys Leu
134              20                  25                  30
136 tgc gcg ggt gtt tgc cgt tgc aaa ctg acc agc agc ggt aaa tgc ccg      144
137 Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys Pro
138          35                  40                  45
140 acc ggt ttt ccg aaa atg att gaa ggt cgt tcg gat gtt gtc cag ctg      192
141 Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Ser Asp Val Val Gln Leu
142      50                  55                  60
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Input Set : **A:\208377.txt**
Output Set: **N:\CRF3\06082001\I864169.raw**

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144 aag aag gac acc ttc gac gac ttc atc aag acg aat gac ctt gtt ctc    240
145 Lys Lys Asp Thr Phe Asp Asp Phe Ile Lys Thr Asn Asp Leu Val Leu
146 65              70                  75                  80
148 gcc gaa ttc ttc gcg ccg tgg tgc ggt cac tgc aag gct ctc gcc ccc    288
149 Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro
150             85                  90                  95
152 gag tac gag gag gct gcg acc aca ctg aag gag aag aac atc aag ctc    336
153 Glu Tyr Glu Glu Ala Ala Thr Thr Leu Lys Glu Lys Asn Ile Lys Leu
154             100                 105                 110
156 gcc aag gtg gac tgc aca gag gag acg gac ctc tgc caa caa cat ggt    384
157 Ala Lys Val Asp Cys Thr Glu Glu Thr Asp Leu Cys Gln Gln His Gly
158         115                 120                 125
160 gtt gag ggc tac ccg act ctc aag gtc ttc cgc ggc ctt gac aac gtc    432
161 Val Glu Gly Tyr Pro Thr Leu Lys Val Phe Arg Gly Leu Asp Asn Val
162     130                 135                 140
164 tcc ccc tac aag ggc cag cgc aag gct gct gct atc acc tcg tac atg    480
165 Ser Pro Tyr Lys Gly Gln Arg Lys Ala Ala Ala Ile Thr Ser Tyr Met
166 145                 150                 155                 160
168 atc aag cag tct ctg ccc gcc gtg tcc gag gtc acg aag gac aac ctg    528
169 Ile Lys Gln Ser Leu Pro Ala Val Ser Glu Val Thr Lys Asp Asn Leu
170                 165                 170                 175
172 gag gag ttc aag aag gcc gac aag gcc gtc ctt gtc gcc tat gtg gat    576
173 Glu Glu Phe Lys Lys Ala Asp Lys Ala Val Leu Val Ala Tyr Val Asp
174             180                 185                 190
176 gct tcc gac aag gcg tcc agt gag gtt ttc acc cag gtc gcc gag aag    624
177 Ala Ser Asp Lys Ala Ser Ser Glu Val Phe Thr Gln Val Ala Glu Lys
178         195                 200                 205
180 ctg cgc gac aac tac ccg ttc ggc tcc agc agc gat gct gcg ctg gcc    672
181 Leu Arg Asp Asn Tyr Pro Phe Gly Ser Ser Ser Asp Ala Ala Leu Ala
182     210                 215                 220
184 gag gct gag ggc gtc aag gct ccc gct atc gtc ctt tac aag gac ttt    720
185 Glu Ala Glu Gly Val Lys Ala Pro Ala Ile Val Leu Tyr Lys Asp Phe
186 225                 230                 235                 240
188 gat gag ggc aag gcg gtc ttc tcc gag aag ttc gag gtg gag gcg atc    768
189 Asp Glu Gly Lys Ala Val Phe Ser Glu Lys Phe Glu Val Glu Ala Ile
190             245                 250                 255
192 gag aag ttc gcc aag acg ggc gcc acc ccg ctc att ggc gag att ggc    816
193 Glu Lys Phe Ala Lys Thr Gly Ala Thr Pro Leu Ile Gly Glu Ile Gly
194             260                 265                 270
196 ccc gaa acc tac tcc gac tac atg tcg gcc ggc atc cct ctg gcc tac    864
197 Pro Glu Thr Tyr Ser Asp Tyr Met Ser Ala Gly Ile Pro Leu Ala Tyr
198             275                 280                 285
200 att ttc gcc gaa acg gcc gag gag cgg aag gag ctc agc gac aag ctc    912
201 Ile Phe Ala Glu Thr Ala Glu Glu Arg Lys Glu Leu Ser Asp Lys Leu
202     290                 295                 300
204 aag ccg atc gcc gag gct cag cgc ggc gtc att aac ttt ggt act att    960
205 Lys Pro Ile Ala Glu Ala Gln Arg Gly Val Ile Asn Phe Gly Thr Ile
206 305                 310                 315                 320
208 gac gcc aag gct ttt ggt gcc cac gcc ggc aac ctg aac ctg aag acc    1008
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Input Set : A:\208377.txt
Output Set: N:\CRF3\06082001\I864169.raw

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209 Asp Ala Lys Ala Phe Gly Ala His Ala Gly Asn Leu Asn Leu Lys Thr
210             325             330             335
212 gac aag ttc ccc gcc ttc gcc atc cag gag gtc gcc aag aac cag aag    1056
213 Asp Lys Phe Pro Ala Phe Ala Ile Gln Glu Val Ala Lys Asn Gln Lys
214             340             345             350
216 ttc ccc ttc gat cag gag aag gag atc acc ttc gag gcg atc aag gct    1104
217 Phe Pro Phe Asp Gln Glu Lys Glu Ile Thr Phe Glu Ala Ile Lys Ala
218             355             360             365
220 ttc gtc gac gac ttt gtc gcc ggt aag atc gag ccc agc atc aag tcg    1152
221 Phe Val Asp Asp Phe Val Ala Gly Lys Ile Glu Pro Ser Ile Lys Ser
222     370             375             380
224 gag ccg atc cct gag aag cag gag ggc ccc gtc acc gtc gtc gtt gcc    1200
225 Glu Pro Ile Pro Glu Lys Gln Glu Gly Pro Val Thr Val Val Val Ala
226 385             390             395             400
228 aag aac tac aat gag atc gtc ctg gac gac acc aag gat gtg ctg att    1248
229 Lys Asn Tyr Asn Glu Ile Val Leu Asp Asp Thr Lys Asp Val Leu Ile
230             405             410             415
232 gag ttc tac gcc ccg tgg tgc ggc cac tgc aag gcc ctg gct ccc aag    1296
233 Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Lys
234             420             425             430
236 tac gag gag ctc ggc gcc ctg tat gcc aag agc gag ttc aag gac cgg    1344
237 Tyr Glu Glu Leu Gly Ala Leu Tyr Ala Lys Ser Glu Phe Lys Asp Arg
238             435             440             445
240 gtc gtc atc gcc aag gtt gat gcc acg gcc aac gac gtt ccc gat gag    1392
241 Val Val Ile Ala Lys Val Asp Ala Thr Ala Asn Asp Val Pro Asp Glu
242     450             455             460
244 atc cag gga ttc ccc acc atc aag ctg tac ccg gcc ggt gcc aag ggt    1440
245 Ile Gln Gly Phe Pro Thr Ile Lys Leu Tyr Pro Ala Gly Ala Lys Gly
246 465             470             475             480
248 cag ccc gtc acc tac tct ggc tcg cgc act gtc gag gac ctc atc aag    1488
249 Gln Pro Val Thr Tyr Ser Gly Ser Arg Thr Val Glu Asp Leu Ile Lys
250             485             490             495
252 ttc atc gcc gag aac ggc aag tac aag gcc gcc atc tcg gag gat gcc    1536
253 Phe Ile Ala Glu Asn Gly Lys Tyr Lys Ala Ala Ile Ser Glu Asp Ala
254             500             505             510
256 gag gag acg tcg tcc gca acc gag acg acc acc gag acg gcc acc aag    1584
257 Glu Glu Thr Ser Ser Ala Thr Glu Thr Thr Thr Glu Thr Ala Thr Lys
258             515             520             525
260 tcg gag gag gct gcc aag gag acg gcg acg gag cac gac gag ctc tga    1632
261 Ser Glu Glu Ala Ala Lys Glu Thr Ala Thr Glu His Asp Glu Leu
262     530             535             540
264 tag gat ccg gct gct aa                                              1649
265     Asp Pro Ala Ala
266     545
269 <210> SEQ ID NO: 5
270 <211> LENGTH: 543
271 <212> TYPE: PRT
272 <213> ORGANISM: Hordeum vulgare
274 <400> SEQUENCE: 5
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277 1               5                   10              15
280 Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys Leu
281         20                  25                  30
284 Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys Pro
285         35                  40                  45
288 Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Ser Asp Val Val Gln Leu
289     50                  55                  60
292 Lys Lys Asp Thr Phe Asp Asp Phe Ile Lys Thr Asn Asp Leu Val Leu
293 65                  70                  75                  80
296 Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro
297                 85                  90                  95
300 Glu Tyr Glu Glu Ala Ala Thr Thr Leu Lys Glu Lys Asn Ile Lys Leu
301             100                 105                 110
304 Ala Lys Val Asp Cys Thr Glu Glu Thr Asp Leu Cys Gln Gln His Gly
305         115                 120                 125
308 Val Glu Gly Tyr Pro Thr Leu Lys Val Phe Arg Gly Leu Asp Asn Val
309     130                 135                 140
312 Ser Pro Tyr Lys Gly Gln Arg Lys Ala Ala Ala Ile Thr Ser Tyr Met
313 145                 150                 155                 160
316 Ile Lys Gln Ser Leu Pro Ala Val Ser Glu Val Thr Lys Asp Asn Leu
317                 165                 170                 175
320 Glu Glu Phe Lys Lys Ala Asp Lys Ala Val Leu Val Ala Tyr Val Asp
321             180                 185                 190
324 Ala Ser Asp Lys Ala Ser Ser Glu Val Phe Thr Gln Val Ala Glu Lys
325         195                 200                 205
328 Leu Arg Asp Asn Tyr Pro Phe Gly Ser Ser Ser Asp Ala Ala Leu Ala
329     210                 215                 220
332 Glu Ala Glu Gly Val Lys Ala Pro Ala Ile Val Leu Tyr Lys Asp Phe
333 225                 230                 235                 240
336 Asp Glu Gly Lys Ala Val Phe Ser Glu Lys Phe Glu Val Glu Ala Ile
337                 245                 250                 255
340 Glu Lys Phe Ala Lys Thr Gly Ala Thr Pro Leu Ile Gly Glu Ile Gly
341             260                 265                 270
344 Pro Glu Thr Tyr Ser Asp Tyr Met Ser Ala Gly Ile Pro Leu Ala Tyr
345             275                 280                 285
348 Ile Phe Ala Glu Thr Ala Glu Glu Arg Lys Glu Leu Ser Asp Lys Leu
349     290                 295                 300
352 Lys Pro Ile Ala Glu Ala Gln Arg Gly Val Ile Asn Phe Gly Thr Ile
353 305                 310                 315                 320
356 Asp Ala Lys Ala Phe Gly Ala His Ala Gly Asn Leu Asn Leu Lys Thr
357                 325                 330                 335
360 Asp Lys Phe Pro Ala Phe Ala Ile Gln Glu Val Ala Lys Asn Gln Lys
361             340                 345                 350
364 Phe Pro Phe Asp Gln Glu Lys Glu Ile Thr Phe Glu Ala Ile Lys Ala
365             355                 360                 365
368 Phe Val Asp Asp Phe Val Ala Gly Lys Ile Glu Pro Ser Ile Lys Ser
369     370                 375                 380
372 Glu Pro Ile Pro Glu Lys Gln Glu Gly Pro Val Thr Val Val Val Ala
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Input Set : **A:\208377.txt**
Output Set: **N:\CRF3\06082001\I864169.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date